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RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/762,759

TIME: 14:40:54

Input Set : N:\Crf3\RULE60\10762759.raw.txt

Output Set: N:\CRF4\08302004\J762759.raw

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1 <110> APPLICANT: Mathur, Brian
2   Turner, C. Alexander Jr.
3   Abuin, Alejandro
4   Friedrich, Glenn
5   Zambrowicz, Brian
6   Sands, Arthur T.
7 <120> TITLE OF INVENTION: Novel Human Kinase Protein and
8   Polynucleotides Encoding the Same
9 <130> FILE REFERENCE: LEX-0083-USA
10 <140> CURRENT APPLICATION NUMBER: US/10/762,759
11 <141> CURRENT FILING DATE: 2004-01-22
12 <150> PRIOR APPLICATION NUMBER: US/09/707,121
13 <151> PRIOR FILING DATE: 2000-11-06
14 <150> PRIOR APPLICATION NUMBER: US 60/164,289
15 <151> PRIOR FILING DATE: 1999-11-08
16 <160> NUMBER OF SEQ ID NOS: 2
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2682
21 <212> TYPE: DNA
22 <213> ORGANISM: homo sapiens
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25   catgatgttt ttggaagcaa tggacttcct ctcacaccaa attccatcaa aattttaggg 120
26   cgctttcaaa tccttaaaac catcacccat cccagactct gccagtatgt ggatatttct 180
27   aggggaaagc atgaacgact agtggtcgtg gctgaacatt gtgaacgtag tctggaagac 240
28   ttgcttcgag aaaggaaacc tgtgagctgt tcaacggttt tgtgtatagc atttgagggt 300
29   cttcagggct tgcagtatat gaacaaacat ggtatagtac acagggcatt gtctcctcat 360
30   aatatcctgt tggaccgaaa gggacatatt aaattggcta aatttggact ttatcacatg 420
31   acagctcatg gtgatgatgt tgatttccca atagggatc cctcgtactt ggcccctgag 480
32   gtaattgcac aggggaatttt caaaaccact gatcacatgc caagtaaaaa accattgcct 540
33   tctggcccca aatcagatgt atggctctctt ggaatcattt tatttgagct ttgtgtggga 600
34   agaâaattat ttcagagctt ggatatttct gaaagactaa aatttttgct tactttggat 660
35   tgtgtagatg acactttaat agttctggct gaagagcatg gttgtttgga cattataaag 720
36   gagcttcctg aaactgtgat agatcttttg aataagtgcc ttaccttcca tccttctaag 780
37   aggccaaccc cagatgaatt aatgaaggac aaagtattca gtgaggtatc acctttatat 840
38   acccccttta ccaaacctgc cagtctgttt tcattctctc tgagatgtgc tgatttaact 900
39   ctgcctgagg atatcagtc gttgtgtaaa gatataaata atgattacct ggcagaaaga 960
40   tctattgaag aagtgtatta cttttggtgt ttggtctggag gtgacttgga gaaagagctt 1020
41   gtcaacaagg aaatcattcg atccaaacca cctatctgca cactcccaa tttctcttt 1080
42   gaggatggtg aaagctttgg acaaggtcga gatagaagct cgcttttaga tgataccact 1140
43   gtgacattgt cgttatgcc gctaagaaat agattgaaag atgttggtgg agaagcattt 1200
44   taccattac ttgaagatga ccagtctaat ttacctcatt caaacagcaa taatgagttg 1260

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45 tctgcagctg ccacgctccc tttaatcatc agagagaagg atacagagta ccaactaaat 1320
46 agaattattc tcttcgacag gctgctaaag gcttatccat ataaaaaaaa ccaaatctgg 1380
47 aaagaagcaa gagttgacat tcctcctctt atgagagggt taacctgggc tgctcttctg 1440
48 ggagttgagg gagctattca tgccaagtac gatgcaattg ataaagacac tccaattcct 1500
49 acagatagac aaattgaagt ggatattcct cgctgtcatc agtacgatga actgttatca 1560
50 tcaccagaag gtcatgcaaa atttaggcgt gtattaaaag cctgggtagt gtctcatcct 1620
51 gatcttggtg attggcaagg tcttgactca ctttgtgctc cattcctata tctaaacttc 1680
52 aataatgaag ccttggctta tgcatgtatg tctgctttta ttcccaaata cctgtataac 1740
53 ttcttcttaa aagacaactc acatgtaata caagagtatc tgactgtctt ctctcagatg 1800
54 attgcatttc atgatccaga gctgagtaat catctcaatg agattgggtt cattccagat 1860
55 ctctatgcca tccttgggtt tcttaccatg tttactcatg tatttccact acacaaaatt 1920
56 ttccacctct gggatacctt actacttggg aattcctctt tcccattctg tattggagta 1980
57 gcaattcttc agcagctgcg ggaccggcgt ttggctaatt gctttaatga gtgtattctt 2040
58 ctcttctccg atttaccaga aattgacatt gaacgctgtg tgagagaatc tatcaacctg 2100
59 ttttgttgga ctctataaag tgctacttac agacagcatg ctcaacctcc aaagccatct 2160
60 tctgacagca gtggaggcag aagttcgga ccttatttct ctgctgagtg tccagatcct 2220
61 ccaaagacag atctgtcaag agaattccatc ccattaaatg acctgaagtc agaagtatca 2280
62 ccacggattt cagcagagga cctgattgac ttgtgtgagc tcacagtgc aggccacttc 2340
63 aaaacaccca gcaagaaaac aaagtccagt aaaccaaagc tcctgggtggg tgacatccgg 2400
64 aatagtgaag actttattcg tggtcacatt tcaggaagca tcaacattcc attcagtgc 2460
65 gccttctactg cagaagggga gcttaccag ggcccttaca ctgctatgct ccagaacttc 2520
66 aaaggggaagg tcattgtcat cgtggggcat gtggcaaac acacagctga gtttcagct 2580
67 caccttgatga agatgaaata tccaagaatc tgtattctag atggtggcat taataaaata 2640
68 aagccaacag gcctcctcac catcccatct cctcaaatat ga 2682

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70 <210> SEQ ID NO: 2

71 <211> LENGTH: 893

72 <212> TYPE: PRT

73 <213> ORGANISM: homo sapiens

74 <400> SEQUENCE: 2

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75 Met Phe Pro Leu Lys Asp Ala Glu Met Gly Ala Phe Thr Phe Phe Ala
76 1 5 10 15
77 Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu Pro Leu Thr
78 20 25 30
79 Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu Lys Thr Ile
80 35 40 45
81 Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg Gly Lys His
82 50 55 60
83 Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser Leu Glu Asp
84 65 70 75 80
85 Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val Leu Cys Ile
86 85 90 95
87 Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys His Gly Ile
88 100 105 110
89 Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp Arg Lys Gly
90 115 120 125
91 His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr Ala His Gly
92 130 135 140
93 Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu Ala Pro Glu
94 145 150 155 160

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95 Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met Pro Ser Lys
96                               165                               170                               175
97 Lys Pro Leu Pro Ser Gly Pro Lys Ser Asp Val Trp Ser Leu Gly Ile
98                               180                               185                               190
99 Ile Leu Phe Glu Leu Cys Val Gly Arg Lys Leu Phe Gln Ser Leu Asp
100                               195                               200                               205
101 Ile Ser Glu Arg Leu Lys Phe Leu Leu Thr Leu Asp Cys Val Asp Asp
102                               210                               215                               220
103 Thr Leu Ile Val Leu Ala Glu Glu His Gly Cys Leu Asp Ile Ile Lys
104                               225                               230                               235                               240
105 Glu Leu Pro Glu Thr Val Ile Asp Leu Leu Asn Lys Cys Leu Thr Phe
106                               245                               250                               255
107 His Pro Ser Lys Arg Pro Thr Pro Asp Glu Leu Met Lys Asp Lys Val
108                               260                               265                               270
109 Phe Ser Glu Val Ser Pro Leu Tyr Thr Pro Phe Thr Lys Pro Ala Ser
110                               275                               280                               285
111 Leu Phe Ser Ser Ser Leu Arg Cys Ala Asp Leu Thr Leu Pro Glu Asp
112                               290                               295                               300
113 Ile Ser Gln Leu Cys Lys Asp Ile Asn Asn Asp Tyr Leu Ala Glu Arg
114                               305                               310                               315                               320
115 Ser Ile Glu Glu Val Tyr Tyr Leu Trp Cys Leu Ala Gly Gly Asp Leu
116                               325                               330                               335
117 Glu Lys Glu Leu Val Asn Lys Glu Ile Ile Arg Ser Lys Pro Pro Ile
118                               340                               345                               350
119 Cys Thr Leu Pro Asn Phe Leu Phe Glu Asp Gly Glu Ser Phe Gly Gln
120                               355                               360                               365
121 Gly Arg Asp Arg Ser Ser Leu Leu Asp Asp Thr Thr Val Thr Leu Ser
122                               370                               375                               380
123 Leu Cys Gln Leu Arg Asn Arg Leu Lys Asp Val Gly Gly Glu Ala Phe
124                               385                               390                               395                               400
125 Tyr Pro Leu Leu Glu Asp Asp Gln Ser Asn Leu Pro His Ser Asn Ser
126                               405                               410                               415
127 Asn Asn Glu Leu Ser Ala Ala Ala Thr Leu Pro Leu Ile Ile Arg Glu
128                               420                               425                               430
129 Lys Asp Thr Glu Tyr Gln Leu Asn Arg Ile Ile Leu Phe Asp Arg Leu
130                               435                               440                               445
131 Leu Lys Ala Tyr Pro Tyr Lys Lys Asn Gln Ile Trp Lys Glu Ala Arg
132                               450                               455                               460
133 Val Asp Ile Pro Pro Leu Met Arg Gly Leu Thr Trp Ala Ala Leu Leu
134                               465                               470                               475                               480
135 Gly Val Glu Gly Ala Ile His Ala Lys Tyr Asp Ala Ile Asp Lys Asp
136                               485                               490                               495
137 Thr Pro Ile Pro Thr Asp Arg Gln Ile Glu Val Asp Ile Pro Arg Cys
138                               500                               505                               510
139 His Gln Tyr Asp Glu Leu Leu Ser Ser Pro Glu Gly His Ala Lys Phe
140                               515                               520                               525
141 Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr
142                               530                               535                               540
143 Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe

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144	545	550	555	560
145	Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys			
146		565	570	575
147	Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu			
148		580	585	590
149	Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu			
150		595	600	605
151	Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile			
152		610	615	620
153	Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile			
154		625	630	635
155	Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe			
156		645	650	655
157	Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg Leu Leu Ala			
158		660	665	670
159	Asn Gly Phe Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu Pro Glu Ile			
160		675	680	685
161	Asp Ile Glu Arg Cys Val Arg Glu Ser Ile Asn Leu Phe Cys Trp Thr			
162		690	695	700
163	Pro Lys Ser Ala Thr Tyr Arg Gln His Ala Gln Pro Pro Lys Pro Ser			
164		705	710	715
165	Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu			
166		725	730	735
167	Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu			
168		740	745	750
169	Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu			
170		755	760	765
171	Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser			
172		770	775	780
173	Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val Asp Ile Arg			
174		785	790	795
175	Asn Ser Glu Asp Phe Ile Arg Gly His Ile Ser Gly Ser Ile Asn Ile			
176		805	810	815
177	Pro Phe Ser Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr Gln Gly Pro			
178		820	825	830
179	Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val			
180		835	840	845
181	Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys			
182		850	855	860
183	Met Lys Tyr Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile Asn Lys Ile			
184		865	870	875
185	Lys Pro Thr Gly Leu Leu Thr Ile Pro Ser Pro Gln Ile			
186		885	890	

VERIFICATION SUMMARY

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